

SEQUENCE LISTING

<110> McCall, Catherine A.
Tang, Liang
Heska Corporation

<120> COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND
CANINE IL-13 RECEPTORS

<130> AL-7

<140> not yet assigned

<141> 2001-04-09

<150> 60/195,659

<151> 2000-04-07

<150> 60/195,874

<151> 2000-04-07

<160> 104

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Canis familiaris

<220>

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<222> (1)..(51)

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1

5

10

15

cct

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Pro

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<212> PRT

<213> Canis familiaris

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 Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val Thr Val
 195 200 205
 Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His
 210 215 220
 Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg
 225 230 235 240
 Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro
 245 250 255
 Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr
 260 265 270
 Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp
 275 280 285
 Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr
 290 295 300
 Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val
 305 310 315 320
 Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu
 325 330 335
 Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg
 340 345 350
 Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val
 355 360 365
 Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile
 370 375 380
 Thr Cys Leu Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp
 385 390 395 400
 Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro
 405 410 415

T06040: 3663660

Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser
 420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val
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Met His Glu Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His
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Ser Pro Gly Lys
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 ctccccaga ctccaccaac tgcacctcac cctggacacc ttttaaaata acgacaagga 1560
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tca 51
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 1 5 10 15

Ser

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 <212> DNA
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<222> (48)..(1457)

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Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly

5

10

15

gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg 152

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly

20

25

30

35

tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat 200

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr

40

45

50

ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc 248

Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val

55

60

65

gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag 296

Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys

70

75

80

ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc 344

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu

85

90

95

cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg 392

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val

100

105

110

115

acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat 440

Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn

120

125

130

ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt 488

Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val

135

140

145

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc 536

Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala

150

155

160

ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc	584
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser	
165 170 175	
tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc	632
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val	
180 185 190 195	
ctg cag tcc tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc	680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro	
200 205 210	
tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg	728
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro	
215 220 225	
gcc agc aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc	776
Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys	
230 235 240	
aag tgt ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg	824
Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser	
245 250 255	
gtc ttc atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga	872
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg	
260 265 270 275	
aca ccc gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct	920
Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro	
280 285 290	
gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc	968
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala	
295 300 305	
aag acg cag cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc	1016
Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val	
310 315 320	
agc gtc ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc	1064
Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe	
325 330 335	
aag tgc aga gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act	1112
Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr	
340 345 350 355	

atc tcc aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg 1160
 Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu
 360 365 370

cca cca tcc cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc 1208
 Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr
 375 380 385

tgc ctg atc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag 1256
 Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln
 390 395 400

agc aat gga cag ccg gag ccc gag agc aag tac cac acg act gcg ccc 1304
 Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro
 405 410 415

cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg 1352
 Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
 420 425 430 435

gac aag agc cgc tgg cag cag gga gac acc ttc aca tgt gcg gtg atg 1400
 Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met
 440 445 450

cat gaa gct cta cag aac cac tac aca gat cta tcc ctc tcc cat tct 1448
 His Glu Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser
 455 460 465

ccg ggt aaa tga 1460
 Pro Gly Lys
 470

<210> 11
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 <212> PRT
 <213> Canis familiaris

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 20 25 30
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
 35 40 45

Ser	Asp	Tyr	Gly	Met	Ser	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	50	55	60	
Gln	Trp	Val	Ala	Ala	Val	Ser	Asn	Arg	Gly	Asp	Thr	Tyr	Tyr	Ala	Asp	65	70	75	80
Ala	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	85	90	95	
Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Ile	Tyr	100	105	110	
His	Cys	Val	Thr	Gly	Val	Trp	Pro	Arg	His	Tyr	Tyr	Gly	Met	Asp	His	115	120	125	
Trp	Gly	Asn	Gly	Thr	Ser	Leu	Phe	Val	Ser	Ser	Ala	Ser	Thr	Thr	Ala	130	135	140	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Cys	Gly	Ser	Thr	Ser	Gly	Ser	145	150	155	160
Thr	Val	Ala	Leu	Ala	Cys	Leu	Val	Ser	Gly	Tyr	Phe	Pro	Glu	Pro	Val	165	170	175	
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ser	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	180	185	190	
Pro	Ser	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Thr	Val	195	200	205	
Thr	Val	Pro	Ser	Ser	Arg	Trp	Pro	Ser	Glu	Thr	Phe	Thr	Cys	Asn	Val	210	215	220	
Val	His	Pro	Ala	Ser	Asn	Thr	Lys	Val	Asp	Lys	Pro	Val	Pro	Lys	Glu	225	230	235	240
Ser	Thr	Cys	Lys	Cys	Ile	Ser	Pro	Cys	Pro	Val	Pro	Glu	Ser	Leu	Gly	245	250	255	
Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Ile	Leu	Arg	260	265	270	
Ile	Thr	Arg	Thr	Pro	Glu	Ile	Thr	Cys	Val	Val	Leu	Asp	Leu	Gly	Arg	275	280	285	
Glu	Asp	Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Gly	Lys	Glu	Val	290	295	300	

His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr
 305 310 315 320

Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly
 325 330 335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile
 340 345 350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
 355 360 365

Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val
 370 375 380

Thr Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val
 385 390 395 400

Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr
 405 410 415

Thr Ala Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
 420 425 430

Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys
 435 440 445

Ala Val Met His Glu Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu
 450 455 460

Ser His Ser Pro Gly Lys
 465 470

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caccaggtct ccccagact ccaccagttg cacctcacc tggacacctt ttaaaataga 1380
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 Gly Cys Gly Leu
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 1 5 10 15

Gly Cys Gly Leu
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<210> 15
<211> 60
<212> DNA
<213> Canis familiaris

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Val Phe Leu Val Ala Ile Leu Lys Gly Val Gln Gly Asp Val Gln Leu
10 15 20

gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg tcc ttg aga ctg 148
Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly Ser Leu Arg Leu
25 30 35

tcc tgt gtg gcc tct gga ttc acc ttt agt agc tgt gcc atg agc tgg 196
Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Cys Ala Met Ser Trp
40 45 50 55

gtc cgt cag tct cca ggg aag ggg cct cag tgg gtc gca act att cgg 244
Val Arg Gln Ser Pro Gly Lys Gly Pro Gln Trp Val Ala Thr Ile Arg
60 65 70

tcg	gtc	ttc	atc	ttt	ccc	cca	aaa	ccc	aag	gac	atc	ctc	gtg	act	gcc	868
Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Ile	Leu	Val	Thr	Ala	
265						270			275							
cgg	aca	ccc	aca	gtc	act	tgt	gtg	gtg	gtg	gat	ctg	gac	cca	gaa	aac	916
Arg	Thr	Pro	Thr	Val	Thr	Cys	Val	Val	Val	Asp	Leu	Asp	Pro	Glu	Asn	
280			285			290						295				
cct	gag	gtg	cag	atc	agc	tgg	ttc	gtg	gat	agt	aag	cag	gtg	caa	aca	964
Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Ser	Lys	Gln	Val	Gln	Thr	
			300			305						310				
gcc	aac	acg	cag	cct	cgt	gag	gag	cag	tcc	aat	ggc	acc	tac	cgt	gtg	1012
Ala	Asn	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Ser	Asn	Gly	Thr	Tyr	Arg	Val	
315						320						325				
gtc	agt	gtc	ctc	ccc	att	ggg	cac	cag	gac	tgg	ctt	tca	ggg	aag	cag	1060
Val	Ser	Val	Leu	Pro	Ile	Gly	His	Gln	Asp	Trp	Leu	Ser	Gly	Lys	Gln	
330						335						340				
ttc	aag	tgc	aaa	gtc	aac	aac	aaa	gcc	ctc	cca	tcc	ccc	att	gag	gag	1108
Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ser	Pro	Ile	Glu	Glu	
345						350						355				
atc	atc	tcc	aag	acc	cca	ggg	cag	gcc	cat	cag	cct	aat	gtg	tat	gtc	1156
Ile	Ile	Ser	Lys	Thr	Pro	Gly	Gln	Ala	His	Gln	Pro	Asn	Val	Tyr	Val	
360			365						370						375	
ctg	ccg	cca	tcg	cgg	gat	gag	atg	agc	aag	aat	acg	gtc	acc	ctg	acc	1204
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Met	Ser	Lys	Asn	Thr	Val	Thr	Leu	Thr	
			380						385						390	
tgt	ctg	gtc	aaa	gac	ttc	ttc	cca	cct	gag	att	gat	gtg	gag	tgg	cag	1252
Cys	Leu	Val	Lys	Asp	Phe	Phe	Pro	Pro	Glu	Ile	Asp	Val	Glu	Trp	Gln	
395						400						405				
agc	aat	gga	cag	cag	gag	cct	gag	agc	aag	tac	cgc	atg	acc	ccg	ccc	1300
Ser	Asn	Gly	Gln	Gln	Glu	Pro	Glu	Ser	Lys	Tyr	Arg	Met	Thr	Pro	Pro	
410						415						420				
cag	ctg	gat	gaa	gat	ggg	tcc	tac	ttc	cta	tac	agc	aag	ctc	tcc	gtg	1348
Gln	Leu	Asp	Glu	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Ser	Val	
425						430						435				
gac	aag	agc	cgc	tgg	cag	cgg	gga	gac	acc	ttc	ata	tgt	gcg	gtg	atg	1396
Asp	Lys	Ser	Arg	Trp	Gln	Arg	Gly	Asp	Thr	Phe	Ile	Cys	Ala	Val	Met	
440			445						450						455	

cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct 1444
His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser
460 465 470

ccg ggt aaa tga	1456
Pro Gly Lys	

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Met Glu Ser Val Leu Tyr Trp Val Phe Leu Val Ala Ile Leu Lys Gly
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Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp
 435 440 445

Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr
 450 455 460

Gln Ile Ser Leu Ser His Ser Pro Gly Lys
 465 470

<210> 18
 <211> 1456
 <212> DNA
 <213> Canis familiaris

<220>
 <223> At location 1430, n = unknown

<400> 18
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 gctgtatagg aagtaggacc catcttcatc cagctggggc ggggtcatgc ggtacttgct 180
 ctcaggctcc tgctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
 tttgaccaga caggtcaggg tgaccgtatt cttgctcatc tcatccccgc atggcggcag 300
 gacatacaca ttaggctgat gggcctgccc tggggctctg gagatgatct cctcaatggg 360
 ggatgggagg gctttgttgt tgactttgca cttgaactgc ttccctgaaa gccagtcctg 420
 gtgcccattg gggaggacac tgaccacacg gtaggtgcca ttggactgct cctcacgagg 480
 ctgctgtgtg gctgtttgca cctgcttact atccacgaac cagctgatct gcacctcagg 540
 gttttctggg tccagatcca ccaccacaca agtgactgtg ggtgtccggg cagtcacgag 600
 gatgtccttg ggttttgggg gaaagatgaa gaccgaaggc cctcccagca ggccacaacc 660
 tgggcatggg cagttgttac agttacactt gcaactcgcat tctttggcca ctggcttgct 720
 tacttttagtg ttgggtggccg ggtggggccac attgcaggtg aaggtctcgc tggggccacct 780
 gctggagggc actgtcacca tgctgctgag ggagtagagc cctgaggact gcaggacgga 840
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 ggggatgtag cctgacacca ggcaggccag ggccaccgtg gagccggatt gggaccacac 960
 gctggggggc agtgggaaaa ccgagggggc cgtggtggag gctgacgaca cgaagaggga 1020
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 acaataatac acggccgtgt cctcggtctt caggctgttc atctgcagat acaccgtgtt 1140
 cttggcggtt tctctggaga tgctgaatcg gcccttcaca gcgtctgcgt agtatatatc 1200
 acttccatca taccgaatag ttgcgacca ctgaggcccc ttccctggag actgacggac 1260
 ccagctcatg gcacagctac taaaggtgaa tccagaggcc acacaggaca gtctcaagga 1320
 cccccaggc ttcaccaggt ctccccaga ctccaccagc tgcacgtcac cctggacacc 1380
 ctttaaaata gcgacaagga aaaccagta gagcacagac tccatggtgn tttgtctgtg 1440
 ttgtgcctga gcactt 1456

<210> 19

[illegible][illegible]

DRAFT

acg tgc aaa gtc aac aac aaa gcc ctc cca tcc ccg atc gag agg acc 1108
 Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Arg Thr
 345 350 355

atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg 1156
 Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu
 360 365 370 375

ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc ttg aca tgc 1204
 Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser Leu Thr Cys
 380 385 390

ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag tgg cag agc 1252
 Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu Trp Gln Ser
 395 400 405

aat gga cag cag gag cct gag agc aag tac cgc acg acc ccg ccc cag 1300
 Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln
 410 415 420

ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac 1348
 Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp
 425 430 435

aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg cat 1396
 Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His
 440 445 450 455

gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc cat tct ccg 1444
 Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser His Ser Pro
 460 465 470

ggg aaa tga 1453
 Gly Lys

<210> 20
 <211> 473
 <212> PRT
 <213> Canis familiaris

<400> 20
 Met Glu Ser Val Leu Phe Trp Val Phe Leu Val Thr Ile Leu Lys Gly
 1 5 10 15
 Val Gln Gly Glu Val Arg Leu Val Glu Ser Gly Gly Thr Leu Val Lys
 20 25 30

Protein: 563360

Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe		
		35					40					45					
Arg	Arg	Tyr	Ser	Met	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Ser	Leu		
		50				55					60						
Gln	Trp	Val	Ala	Gly	Ile	Asn	Gly	Asp	Gly	Thr	Gly	Thr	Ser	Tyr	Ser		
		65			70					75					80		
Gln	Thr	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn		
			85					90						95			
Thr	Leu	Tyr	Leu	Gln	Ile	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Ser	Ala	Val		
			100					105						110			
Tyr	Tyr	Cys	Ala	Lys	Ser	Trp	Ser	Arg	Asn	Gly	Asp	Leu	Asp	Tyr	Trp		
		115					120					125					
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Thr	Ala	Pro		
		130				135					140						
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Cys	Gly	Ser	Thr	Ser	Gly	Ser	Thr		
		145			150				155						160		
Val	Ala	Leu	Ala	Cys	Leu	Val	Ser	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr		
				165					170					175			
Val	Ser	Trp	Asn	Ser	Gly	Ser	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro		
			180					185					190				
Ser	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Met	Val	Thr		
		195					200					205					
Val	Pro	Ser	Ser	Arg	Trp	Pro	Ser	Glu	Thr	Phe	Thr	Cys	Asn	Val	Ala		
		210				215					220						
His	Pro	Ala	Ser	Lys	Thr	Lys	Val	Asp	Lys	Pro	Val	Pro	Lys	Arg	Glu		
		225			230				235					240			
Asn	Gly	Arg	Val	Pro	Arg	Pro	Pro	Asp	Cys	Pro	Lys	Cys	Pro	Ala	Pro		
			245					250						255			
Glu	Met	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys		
		260						265					270				
Asp	Thr	Leu	Leu	Ile	Ala	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val		
		275					280					285					

Asp Leu Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp
 290 295 300

Gly Lys Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe
 305 310 315 320

Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp
 325 330 335

Trp Leu Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu
 340 345 350

Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His
 355 360 365

Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys
 370 375 380

Asn Thr Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp
 385 390 395 400

Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys
 405 410 415

Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu
 420 425 430

Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr
 435 440 445

Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 450 455 460

Glu Ser Leu Ser His Ser Pro Gly Lys
 465 470

<210> 21

<211> 1453

<212> DNA

<213> Canis familiaris

<400> 21

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 gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcgtgc ggtacttgct 180

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ctcaggctcc tgctgtccat tgctctgcca ctccacatca atgtcaggtg ggaagaagtc 240
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gacatacaca ctgggctgat gggcttgccc tctggccttg gagatgggtcc tctcgatcgg 360
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gtctttctggg tccagatcca ccaccacaca tgtgacctca ggtgttcggg caatcaagag 600
ggtgtccttg ggtttcgggg gaaagatgaa gaccgaaggc cctcccagca tttcaggggc 660
tgggcatttg ggacaatcag gtgggcgagg aactcttcca ttttctcttt tgggcactgg 720
cttgtctact ttagttttgc tggccgggtg ggccacgttg caggtgaagg tctcgctggg 780
ccacctgctg gagggcactg tcaccatgct gctgagggag tagagccctg aggactgcag 840
gacggacggg aaggtgtgca caccgctggt caaggagccg gaattccagg acacagttac 900
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cccgcagctg ggggccagtg ggaaaaccga gggggccgtg gtggaggctg aggagacggt 1020
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ataatacaca gcagagtctt cggctctcag gctgtttatc tgcagataga ggggtgttctt 1140
ggcgttgtct ctggagatgg tgaatcggcc cttcacagtc tgtgaatagg atgttcctgt 1200
gccatcaccg ttaatcccg cgacccactg caggctcttg cctggagcct ggcggaccca 1260
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cccaggcttc accagggttc ctccagactc caccaaactg acctcacctt ggacaccttt 1380
taaaatagtg acaaggaaaa ccagaagag cacagactcc atggtgattt gtctgtgtgg 1440
tgtcctgagc act 1453
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<210> 22
<211> 66
<212> DNA
<213> Canis familiaris
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<220>
<221> CDS
<222> (1)..(66)
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<400> 22
ccc aaa aga gaa aat gga aga gtt cct cgc cca cct gat tgt ccc aaa 48
Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
    1             5             10            15

tgc cca gcc cct gaa atg 66
Cys Pro Ala Pro Glu Met
    20
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<210> 23
<211> 22
<212> PRT
<213> Canis familiaris
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<400> 23

Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
1 5 10 15

Cys Pro Ala Pro Glu Met
20

<210> 24

<211> 66

<212> DNA

<213> Canis familiaris

<400> 24

catttcaggg gctgggcatt tgggacaatc aggtgggcga ggaactcttc cattttctct 60
tttggg 66

<210> 25

<211> 938

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (37)..(753)

<220>

<223> At location 475, n = unknown

<400> 25

ggcacgaggg tccccagaag gcaggatcaa tcagtg atg tcc tcc gac atg gcc 54
Met Ser Ser Asp Met Ala
1 5

tgg tcc cct ctc ctc ctc aca ctc ctc gct cac tgc aca ggg tcc tgg 102
Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala His Cys Thr Gly Ser Trp
10 15 20

gcc cag gct gtg ttg aat cag ccg gcc tca gta tct ggg gcc ctg ggc 150
Ala Gln Ala Val Leu Asn Gln Pro Ala Ser Val Ser Gly Ala Leu Gly
25 30 35

cag aag gtc acc atc tcc tgc tct gga gac acg aat gac att gat ata 198
Gln Lys Val Thr Ile Ser Cys Ser Gly Asp Thr Asn Asp Ile Asp Ile
40 45 50

ttc ggt gtg aac tgg tac caa caa ctc cca gga aag gcc cct aca gtc	246
Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Thr Val	
55 60 65 70	
ctc gtg gac agt gat ggg gat cga ccc tca ggg gtc cct gac aga ttt	294
Leu Val Asp Ser Asp Gly Asp Arg Pro Ser Gly Val Pro Asp Arg Phe	
75 80 85	
tct ggc tcc agt tct ggc aac tca ggc acc ctg acc atc act ggg ctc	342
Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr Leu Thr Ile Thr Gly Leu	
90 95 100	
cag gct gag gac gag gct gat tat tac tgt cag tct gtt gat tcc acg	390
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Val Asp Ser Thr	
105 110 115	
ctt ggt gtt tac gtg ttc ggc tca gga acc caa ctg act gtc ctt ggt	438
Leu Gly Val Tyr Val Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Gly	
120 125 130	
cag ccc aag gcc tcc ccc tgc gtc aca ctc ttc ccg ncc tyc tyt gag	486
Gln Pro Lys Ala Ser Pro Ser Val Thr Leu Phe Pro Xaa Xaa Xaa Glu	
135 140 145 150	
gag ctc ggc gcc aac aag gcc acc ctg gtg tgc ctc atc agc gac ttc	534
Glu Leu Gly Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe	
155 160 165	
tac ccc arc ggc gtg acg gtg gcc tgg aag gca gac ggc agc ccc gtc	582
Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val	
170 175 180	
acc cag ggc gtg gag acc acc aag ccc tcc aag cag agc aac aac aag	630
Thr Gln Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys	
185 190 195	
tac gcg gcc agc agc tac ctg agc ctg acg cct gac aag tgg aaa tct	678
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Asp Lys Trp Lys Ser	
200 205 210	
cac agc agc ttc agc tgc ctg gtc acg cat gag ggg agc ccc gtg gaa	726
His Ser Ser Phe Ser Cys Leu Val Thr His Glu Gly Ser Pro Val Glu	
215 220 225 230	
aaa aag gtg gcc ccc gca aag tgc tct taggttcccg atgccccccg	773
Lys Lys Val Ala Pro Ala Lys Cys Ser	
235	

[illegible]

29

180

185

190

Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr
 195 200 205

Pro Asp Lys Trp Lys Ser His Ser Ser Phe Ser Cys Leu Val Thr His
 210 215 220

Glu Gly Ser Pro Val Glu Lys Lys Val Ala Pro Ala Lys Cys Ser
 225 230 235

<210> 27

<211> 938

<212> DNA

<213> Canis familiaris

<220>

<223> At location 464, n = unknown

<400> 27

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aagatcctcc tggaggtcct gaggtcttga gccccctttg gtgggcgggg ggcacgagg 180
acctaagagc actttgcggg ggccaccttt tttccacgg ggctcccctc atgcgtgacc 240
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gccgcgtact tgttggtgct ctgcttgagg ggcttggtgg tctccacgcc ctgggtgacg 360
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cacaccaggg tggccttggt ggccgccgagc tcctcaragr agnccgggaa gagtgtgacc 480
gagggggagg ccttgggctg accaaggaca gtcagttggg ttcctgagcc gaacacgtaa 540
acaccaagcg tggaatcaac agactgacag taataatcag cctcgtcctc agcctggagc 600
ccagtgatgg tcagggtgcc tgagttgcca gaactggagc cagaaaatct gtcagggacc 660
cctgagggtc gatccccatc actgtccacg aggactgtag gggcctttcc tgggagttgt 720
tggtaccagt tcacaccgaa tatatcaatg tcattcgtgt ctccagagca ggagatggtg 780
accttctggc ccagggcccc agatactgag gccggctgat tcaacacagc ctggggccag 840
gaccctgtgc agtgagcgag gagtgtgagg aggagagggg accaggccat gtcggaggac 900
atcactgatt gatcctgcct tctggggacc ctctgtgcc 938

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<210> 28

<211> 578

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(423)

<220>

<223> At locations 471, 481, 522 and 549, n = unknown

<400> 28

cat caa gat tgg ttt aat ggt aag gag ttc aaa tgt aga gtc aac cac 48
His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His
1 5 10 15

ata gac ctc ccg tct ccc atc gag agg acc atc tct aag gcc aga ggg 96
Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
20 25 30

agg gcc cat aag ccc agt gtg tat gtc ctg ccg cca tcc cca aag gag 144
Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
35 40 45

ttg tca tcc agt gac aca gtc agc atc acc tgc ctg ata aaa gac ttc 192
Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe
50 55 60

tac cca cct gac att gat gtg gag tgg cag agc aat gga cag cag gag 240
Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
65 70 75 80

cct gag agc aag tac cgc acg acc ccg ccc cag ctg gac gag gac ggg 288
Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly
85 90 95

tcc tac ttc ctg tac agc aag ctc tct gtg gac aag agc cgc tgg cag 336
Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
100 105 110

cgg gga gac acc ttc ata tgt gcg gtg atg cat gaa gct cta cac aac 384
Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn
115 120 125

cac tac aca cag aaa tcc ctc tcc cat tct ccg ggt aaa tgagcaacac 433
His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys
130 135 140

gcccgccacc cagcaagccc cccacccttg gctctcanga tccctganga cacctgagcc 493

cctgtccctg tgtacataac cctgggtang cacccatcat gaaataaagc acccancact 553

gccttgggcc cttgcaaaaa aaaaa 578

"GCGC" 5533333333

<210> 29
 <211> 141
 <212> PRT
 <213> Canis familiaris
 <223> At locations 471, 481, 522 and 549, n = unknown

<400> 29
 His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His
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 Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
 20 25 30
 Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
 35 40 45
 Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe
 50 55 60
 Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
 65 70 75 80
 Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly
 85 90 95
 Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
 100 105 110
 Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn
 115 120 125
 His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys
 130 135 140

<210> 30
 <211> 578
 <212> DNA
 <213> Canis familiaris
 <220>
 <223> At locations 30, 57, 98 and 108, n = unknown

<400> 30
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 gtgggggggct tgctgggtgc cgggcgtggt gctcatttac ccggagaatg ggagagggat 180

THE PAPER OF THE DAY

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<220>  
<221> CDS  
<222> (59) .. (1183)
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gtg gag tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc 1018
 Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg
 305 310 315 320

acg acc ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc 1066
 Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser
 325 330 335

aag ctc tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata 1114
 Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile
 340 345 350

tgt gcg gtg atg cat gaa gct tta cac aac cac tac aca cag aaa tcc 1162
 Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 355 360 365

ctc tcc cat tct ccg ggt aaa tgagcaacac gcccggcacc cagcaagccc 1213
 Leu Ser His Ser Pro Gly Lys
 370 375

cccacccttg gctttcagga tcccatgagg atgcctgagc ccccatccct gtgtacataa 1273

ccccgggtag gcacctggca tgaaataaag caccagtagc tgccttgga aaaaaaaaaa 1333

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1364

<210> 32

<211> 375

<212> PRT

<213> Canis familiaris

<400> 32

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser
 1 5 10 15

Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln
 20 25 30

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
 35 40 45

Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
 50 55 60

Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
 65 70 75 80

Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile
 340 345 350

Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 355 360 365

Leu Ser His Ser Pro Gly Lys
 370 375

<210> 33
 <211> 1364
 <212> DNA
 <213> Canis familiaris

<400> 33
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 tcaccgcaca tatgaaggtg tctccccgct gccagcggct cttgtccaca gagagcttgc 300
 tgtacaggaa gtaggaccgc tcctcgtcca gctggggcgg ggtcgtgcgg tacttgctct 360
 caggctcctg ctgtccattg ctctgccact ccacatcaat gtcaggtggg aagaagtctt 420
 tgatcaggca tgtcaagctg actgtgttct tgctcaactc ctcccgggat ggcggcagga 480
 catacacact gggttgatgg gcttgccctc tggccttgga gatggctctc tcgattgggg 540
 atgggagggc tttgttggtg actttgcacg tgaactgctt ccccttgagc cagtcctggt 600
 gcccaatggg gaggacactg accacacggg aggtgccatt gaactgctcc tcacgaggct 660
 gagtcttggc tgtttgcatc tgcttaccgt ccacgaacca gctgatctgc acctcagggt 720
 cttctgggtc cagatccacc accacacatg tgacctcagg tgttcgggca atcaagaggg 780
 tgtccttggg tttcggggga aagatgaaga ccgaaggccc tcccagcatt tcagggggtg 840
 ggcatttggg acaatcaggt gggcgaggaa ctcttcatt ttctcttttg ggcactggct 900
 tgtctacttt agttttgctg gccgggtggg ccacgttgca ggtgaaggct tcgctgggcc 960
 acctgctgga gggcactgtc accatgctgc tgaggagta gagccctgag gactgcagga 1020
 cggacgggaa ggtgtgcaca ccgctgggtc aggagccgga attccaggac acagttacag 1080
 gctcggggaa gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc 1140
 cgcagctggg ggccagtggg aaaaccgagg gggccgtggg ggaggctgag gagacggtga 1200
 ccagggttcc ctggccccag gagtcaaaat tcggaccgta ccagttgatc cataaccac 1260
 ttgtacagta atacagggcc gtatcctcag ctctcaggct gttcatctgc agatacagcg 1320
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<210> 34
 <211> 1168
 <212> DNA
 <213> Canis familiaris

<220>

<221> CDS

<222> (48)..(1166)

<400> 34

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                                     Met Glu Ser
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gtg ctc tgc tgg gtt ttc ctt gtc tct att tta aaa ggt gtc cag ggt      104
Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly
      5                      10                      15

gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg      152
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
      20                      25                      30                      35

tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat      200
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr
                      40                      45                      50

ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc      248
Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val
                      55                      60                      65

gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag      296
Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys
      70                      75                      80

ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc      344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
      85                      90                      95

cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg      392
Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val
      100                      105                      110                      115

acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat      440
Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn
                      120                      125                      130

ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt      488
Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
                      135                      140                      145

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc      536
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
      150                      155                      160
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Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe
 180 185 190

Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val
 195 200 205

Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val
 210 215 220

Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu
 225 230 235 240

Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly
 245 250 255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg
 260 265 270

Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg
 275 280 285

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val
 290 295 300

His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr
 305 310 315 320

Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly
 325 330 335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Pro Pro Ser Pro Ile
 340 345 350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
 355 360 365

Tyr Val Leu Pro Pro
 370

<210> 36

<211> 1168

<212> DNA

<213> Canis familiaris

<400> 36

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tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg gcc agc aac 336
Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro Ala Ser Asn
100 105 110

tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg gtc ttc atc 432
Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile
130 135 140

ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc gag 480
Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu
145 150 155 160

atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct gag gtg cag 528
Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln
165 170 175

atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc aag acg cag 576
Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln
180 185 190

cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc agc gtc ctc 624
Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
195 200 205

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ccc att gag cac cag gac tgg ctc acc gga aag gag ttc aag tgc aga    672
Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg
      210              215              220

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gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act atc tcc aaa 720
Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys
225 230 235 240

gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg cca cca tcc 768
Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser
245 250 255

cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc tgc ctg atc 816

85

90

95

Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro Ala Ser Asn
100 105 110

Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys Ile
115 120 125

Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile
130 135 140

Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu
145 150 155 160

Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln
165 170 175

Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln
180 185 190

Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
195 200 205

Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg
210 215 220

Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys
225 230 235 240

Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser
245 250 255

Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile
260 265 270

Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly
275 280 285

Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp
290 295 300

Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser
305 310 315 320

Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Ala
325 330 335

Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys

<210> 39
 <211> 1059
 <212> DNA
 <213> Canis familiaris

<400> 39
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 catcaccgca catgtgaagg ggtctccctg ctgccagcgg ctcttggtcca cagagagctt 120
 gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180
 ctggggctcc ggctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
 tttgatcagg caggtcaggg tgaccgtgtc actggatgac aactcctttg gggatgggtgg 300
 caggacatac aactgggct gatgggcttg ccctctggct ttggagatag tcctctcgat 360
 gggggacggg aggcctatgt ggttgactct gcaattgaac tcctttccgg tgagccagtc 420
 ctggtgctca atggggagga cgctgaccac acggtaggtg ctggtgaact gctgctcacg 480
 aggctgcgtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540
 agggctcctca cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct 600
 gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctccca gtgattcagg 660
 gactgggcat ggggatatac acttgacaggt ggactctttg ggcactggct tgtctacttt 720
 agtggtgctg gccgggtgga ccacgttgca ggtgaaggte tcgctgggcc acctgctgga 780
 gggcactgtc accgtgctgc tgagggagta gagccctgag gactgcagga cggacgggaa 840
 ggtgtgcaca ccgctggtca aggagtcgga attccaggac acagttacag gctcggggaa 900
 gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc cgcagctggg 960
 ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gacacgaaga gtgaggtgcc 1020
 attgccccag tggtcatac cataataatg tcgcgcca 1059

<210> 40
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<220>
 <223> At locations 15 and 21, n = unknown

<400> 40
 caycargayt ggytnaaygg naargartty aartgy 36

<210> 41
 <211> 28

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 41
gccctccagc aggtggccca gcgagacc

28

<210> 42
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 42
ggggatggcg gcaggacata cac

23

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 43
tttaccgga gaatgggaga ggg

23

<210> 44
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 44
ggtctgcgtg ggccacctgc tggagggc

28

<210> 45
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<400> 45
 ggggtggggggg cttgctgggt gccgggcg 28

<210> 46
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<400> 46
 ccaggtgacc ccattcagtg ctcaggacac 30

<210> 47
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<400> 47
 ctgtgtgacg ggagtatggc cgcgac 26

<210> 48
 <211> 483
 <212> DNA
 <213> Canis familiaris

<220>
 <223> At location 470, n = unknown

<400> 48
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 agtcattttg acaacaaaca ggataagaaa attgctcctg aaactcatcg ttcaaaagaa 120
 gtacccttga atgagaggat ttgtctgcaa gtgggggtccc agtgcagcac caatgaaagt 180
 gacaatccta gcatttttgt ggaaaagtgc accccaccac ctgaaggtgg tcctgagtcg 240
 gctgtgactg agctacaatg tgtttggcac aacctgagct acatgaagtg tacttggctt 300
 cctggaagga atacaagccc tgacaccaac tatactctct actattggca cagcagcctg 360
 ggaaaaattc ttcaatgcga agacatctat agagaaggtc aacacattgg ttgttccttt 420
 gctctgacta atttgaagga ttccagtttt gaacaacaca gtgtccagan gatggtcaag 480
 gtt 483

<210> 49
 <211> 1547
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(1215)

<400> 49
 ggc ggg gtc gcc gca ccc acc gaa act cag cca cct gtg acg aat ttg 48
 Gly Gly Val Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu
 1 5 10 15
 agt gtt tct gtt gaa aac ctc tgc acg gtc ata tgg aca tgg aac cct 96
 Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro
 20 25 30
 ccc gag gga gcc agc ccg aat tgc acc tta cgg tat ttt agt cat ttt 144
 Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr Phe Ser His Phe
 35 40 45
 gac aac aaa cag gat aag aaa att gct cct gaa act cat cgt tca aaa 192
 Asp Asn Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr His Arg Ser Lys
 50 55 60
 gaa gta ccc ctg aat gag agg att tgt ctg caa gtg ggg tcc cag tgc 240
 Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys
 65 70 75 80
 agc acc aat gaa agt gac aat cct agc att ttg gtg gaa aag tgc acc 288
 Ser Thr Asn Glu Ser Asp Asn Pro Ser Ile Leu Val Glu Lys Cys Thr
 85 90 95
 cca cca cct gaa ggt gat cct gag tcg gct gtg act gag cta caa tgt 336

Pro	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val	Thr	Glu	Leu	Gln	Cys	
			100					105					110			
gtt	tgg	cac	aac	ctg	agc	tac	atg	aag	tgt	act	tgg	ctt	cct	gga	agg	384
Val	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Thr	Trp	Leu	Pro	Gly	Arg	
		115					120				125					
aat	aca	agc	cct	gac	acc	aac	tat	act	ctc	tac	tat	tgg	cac	agc	agc	432
Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu	Tyr	Tyr	Trp	His	Ser	Ser	
		130				135				140						
ctg	gga	aaa	att	ctt	caa	tgc	gaa	gac	atc	tat	aga	gaa	ggc	caa	cac	480
Leu	Gly	Lys	Ile	Leu	Gln	Cys	Glu	Asp	Ile	Tyr	Arg	Glu	Gly	Gln	His	
145					150				155					160		
att	ggc	tgt	tcc	ttt	gct	ctg	act	aat	ttg	aag	gat	tcc	agt	ttt	gaa	528
Ile	Gly	Cys	Ser	Phe	Ala	Leu	Thr	Asn	Leu	Lys	Asp	Ser	Ser	Phe	Glu	
			165					170						175		
caa	cac	agt	gtc	caa	ata	atg	gtc	aag	gat	aat	gca	aga	aaa	att	aga	576
Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	Ala	Arg	Lys	Ile	Arg	
			180					185					190			
ccg	tcc	ttc	aat	ata	gtg	cct	tta	act	tct	cat	gtg	aaa	cct	gat	ccc	624
Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	His	Val	Lys	Pro	Asp	Pro	
		195				200					205					
ccc	cat	att	aag	cgt	ctc	ttc	ttc	caa	aat	ggc	aac	ttg	tat	gtg	caa	672
Pro	His	Ile	Lys	Arg	Leu	Phe	Phe	Gln	Asn	Gly	Asn	Leu	Tyr	Val	Gln	
	210				215				220							
tgg	aag	aat	cca	caa	aat	ttt	tat	agc	aga	tgc	tta	tct	tac	caa	gta	720
Trp	Lys	Asn	Pro	Gln	Asn	Phe	Tyr	Ser	Arg	Cys	Leu	Ser	Tyr	Gln	Val	
225				230				235						240		
gaa	gtc	aat	aac	agc	cag	act	gag	acg	aat	gat	ata	ttc	tac	gtt	gaa	768
Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	Asn	Asp	Ile	Phe	Tyr	Val	Glu	
			245					250					255			
gaa	gcc	aaa	tgt	cag	aat	tca	gaa	ttt	gag	gga	aac	ctg	gag	ggc	aca	816
Glu	Ala	Lys	Cys	Gln	Asn	Ser	Glu	Phe	Glu	Gly	Asn	Leu	Glu	Gly	Thr	
		260				265					270					
att	tgt	ttc	atg	gtc	ccc	ggc	gtt	ctt	cct	gat	act	ttg	aac	aca	gtc	864
Ile	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro	Asp	Thr	Leu	Asn	Thr	Val	
		275				280					285					
aga	ata	aga	gtc	aga	aca	aat	aag	tta	tgc	tat	gag	gat	gac	aaa	ctc	912

Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu
290 295 300

tgg agt aat tgg agt caa gcg atg agt ata ggt gag aat acc gac ccc 960
Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro
305 310 315 320

acg ttc tat ata acc atg ttg ctc gcc act caa gtc atc gtt gca ggt 1008
Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly
325 330 335

gcc atc ata atc ctt ctg ctt tat ctc aaa agg ctc aag atc att ata 1056
Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile
340 345 350

ttc cct cca att cct gat cct ggc aag att ttt aaa gaa atg ttt gga 1104
Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly
355 360 365

gac cag aat gat gat acg ctg cac tgg agg aag tac gac atc tat gag 1152
Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu
370 375 380

aag caa aca aaa gaa gaa acg gac tca gta gtg ctg att gaa aac ctg 1200
Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu
385 390 395 400

aag aaa gcc tct cag taatggggat aacttatttt agccttcagc atgaccttgt 1255
Lys Lys Ala Ser Gln
405

aaagattcat cccacgttc tcgggaagct tcaaggtcaa gcatcttggg aaaggacatt 1315

acagtttcta cagcatgggtg tacctgggca tctccgacta cttcttcaac acagcagggc 1375

ttgtgtacca agaggcaggg gccttaaaca tgaccatcac ggacgacatg ataccaaaga 1435

aatccaaatt ccgactgaca accgattttt tggggaccct cataccccaa gtggccgaga 1495

tgttccccaa catgacgggt caattcaacg tctgggcctc ctccccgccg ca 1547

<210> 50

<211> 405

<212> PRT

<213> Canis familiaris

<400> 50

Glu Ala Lys Cys Gln Asn Ser Glu Phe Glu Gly Asn Leu Glu Gly Thr
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Ile Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val
 275 280 285

Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu
 290 295 300

Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro
 305 310 315 320

Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly
 325 330 335

Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile
 340 345 350

Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly
 355 360 365

Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu
 370 375 380

Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu
 385 390 395 400

Lys Lys Ala Ser Gln
 405

<210> 51
 <211> 1547
 <212> DNA
 <213> Canis familiaris

<400> 51
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 atcatgtcgt ccgtgatggt catgtttaag gccctgcct cttggtacac aagccctgct 180
 gtgttgaaga agtagtcgga gatgccagg tacaccatgc tgtagaaact gtaatgtcct 240
 ttccaagat gcttgacctt gaagcttccc gagaacgtgg ggatgaatct ttacaaggctc 300
 atgctgaagg ctaaaataag ttatcccat tactgagagg ctttcttcag gttttcaatc 360
 agcactactg agtccgtttc ttcttttggt tgcttctcat agatgtcgta cttcctccag 420
 tgcagcgtat catcattctg gtctccaaac atttctttaa aaatcttgcc aggatcagga 480
 attggaggga atataatgat cttgagcctt ttgagataaa gcagaaggat tatgatggca 540
 cctgcaacga tgacttgagt ggcgagcaac atggttatat agaacgtggg gtcggtattc 600

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tcacctatac tcactgcttg actccaatta ctccagagtt tgtcatcctc atagcataac 660
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atgaaacaaa ttgtaccctc cagggtttccc tcaaattctg aattctgaca tttggcttct 780
tcaacgtaga atatatcatt cgtctcagtc tggctgttat tgacttctac ttggtaagat 840
aagcatctgc tataaaaatt ttgtggattc ttccattgca catacaagtt accatttttg 900
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tcaaaactgg aatccttcaa attagtcaga gcaaaggaac aaccaatgtg ttgaccttct 1080
ctatagatgt cttcgcatg aagaattttt cccaggctgc tgtgccaata gtagagagta 1140
tagttggtgt cagggttctg attccttcca ggaagccaag tacacttcat gtagctcagg 1200
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attttcttat cctgtttgtt gtcaaaatga ctaaaatacc gtaagggtgca attcgggctg 1440
gctccctcgg gaggggtcca tgtccatatg accgtgcaga ggttttcaac agaaacactc 1500
aaattcgtca cagggtggctg agtttcgggt ggtgcggcga ccccgcc 1547

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<210> 52
<211> 1215
<212> DNA
<213> Canis familiaris

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<400> 52
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accttacggt attttagtca ttttgacaac aaacaggata agaaaattgc tcctgaaact 180
catcgttcaa agaagttacc cctgaatgag aggatttgct tgcaagtggg gtcccagtcg 240
agcaccaatg aaagtgcaca tcctagcatt ttgggtggaag agtgcacccc accacctgaa 300
ggtgatcctg agtcggctgt gactgagcta caatgtgttt ggcacaacct gagctacatg 360
aagtgtactt ggcttctctg aaggaatata agccctgaca ccaactatac tctctactat 420
tggcacagca gcctgggaaa aattcttcaa tgcaagaca tctatagaga aggtcaacac 480
attggttgtt ctttctctct gactaatttg aaggattcca gttttgaaca acacagtgtc 540
caaataatgg tcaaggataa tgcaagaaaa attagaccgt cttcaatat agtgccttta 600
acttctcatg tgaaacctga tcccccccat attagcgtc tcttcttcca aaatggtaac 660
ttgtatgtgc aatggaagaa tccacaaaat ttttatagca gatgcttata ttaccaagta 720
gaagtcaata acagccagac tgagacgaat gatataattc acgttgaaga agccaaatgt 780
cagaattcag aatttgaggg aaacctggag ggtacaattt gtttcatggg ccccggcgtt 840
cttctgata ctttgaacac agtcagaata agagtcagaa caaataagtt atgctatgag 900
gatgacaaac tctggagtaa ttggagtcaa gcgatgagta taggtgagaa taccgacccc 960
acgttctata taaccatgtt gctcgccact caagtcacgc ttgcaggtgc catcataatc 1020
cttctgcttt atctcaaaag gctcaagatc attatattcc ctccaattcc tgatcctggc 1080
aagattttta aagaaatgtt tggagaccag aatgatgata cgctgcactg gaggaagtac 1140
gacatctatg agaagcaaac aaaagaagaa acggactcag tagtgctgat tgaaaacctg 1200
aagaaagcct ctcag 1215

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<210> 53

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<211> 1215
 <212> DNA
 <213> Canis familiaris

<400> 53
 ctgagaggct ttcttcaggt tttcaatcag cactactgag tccgtttctt cttttgtttg 60
 cttctcatag atgtcgctact tcctccagtg cagcgtatca tcattctggg ctccaaacat 120
 ttcttttaaaa atcttgccag gatcaggaat tggagggaat ataatgatct tgagcctttt 180
 gagataaagc agaaggatta tgatggcacc tgcaacgatg acttgagtgg cgagcaacat 240
 ggttatatag aacgtggggg cgggtattctc acctatactc atcgcttgac tccaattact 300
 ccagagtttg tcatcctcat agcataactt atttgttctg actcttattc tgactgtgtt 360
 caaagtatca ggaagaacgc cggggaccat gaaacaaatt gtaccctcca ggtttccctc 420
 aaattctgaa ttctgacatt tggcttcttc aacgtagaat atatcattcg tctcagtcgtg 480
 gctgttattg acttctactt ggtaagataa gcatctgcta taaaaatttt gtggattctt 540
 ccattgcaca tacaagttac ctttttgga gaagagacgc ttaatatggg ggggatcagg 600
 tttcacatga gaagttaaag gcactatatt gaaggacggg ctaatttttc ttgcattatc 660
 cttgaccatt atttggacac tgtgttgttc aaaactggaa tccttcaa atagtcagagc 720
 aaaggaacaa ccaatgtgtt gaccttctct atagatgtct tcgcattgaa gaatttttcc 780
 caggctgctg tgccaatagt agagagtata gttggtgtca gggcttgat tccttccagg 840
 aagccaagta cacttcatgt agctcagggt gtgccaaaca cattgtagct cagtcacagc 900
 cgactcagga tcaccttcag gtgggtgggg gcacttttcc accaaaatgc taggattgtc 960
 actttcattg gtgctgcact gggacccac ttgcagacaa atcctctcat tcaggggtac 1020
 ttcttttgaa cgatgagttt caggagcaat tttcttatcc tgtttgttgt caaaatgact 1080
 aaaataccgt aaggtgcaat tcgggctggc tccttcggga gggttccatg tccatagac 1140
 cgtgcagagg ttttcaacag aaacactcaa attcgtcaca ggtggctgag tttcgggtggg 1200
 tgcggcgacc ccgcc 1215

<210> 54
 <211> 620
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (184)..(618)

<400> 54
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 aattaatgtc tccaaactgg agaagagaaa aaaaagagga cctgtgataa ttgcctatga 120
 taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180
 gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt 228
 Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu
 1 5 10 15

gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt 276
 Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val
 20 25 30

aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat 324
 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
 35 40 45

ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa 372
 Leu Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu
 50 55 60

tgc aca ata gaa tat gaa tta aaa tac cga aac att gat agt gaa aac 420
 Cys Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn
 65 70 75

tgg aag acc atc att acc aag aat cta cat tac aaa gat ggg ttt gat 468
 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 80 85 90 95

ctt aac aaa ggt att gaa gca aag ata aac aca ctt ctg cca gca caa 516
 Leu Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln
 100 105 110

tgc aca aat gga tca gaa gtt aga agt tca tgg gca gaa act act tat 564
 Cys Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr
 115 120 125

tgg aca tca cca caa gga aat cgg gaa act aaa att caa gat atg gac 612
 Trp Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp
 130 135 140

tgt gta ta 620
 Cys Val
 145

<210> 55
 <211> 145
 <212> PRT
 <213> Canis familiaris

<400> 55
 Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu Val
 1 5 10 15
 Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn
 20 25 30

Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu
 35 40 45

Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys
 50 55 60

Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp
 65 70 75 80

Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu
 85 90 95

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys
 100 105 110

Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp
 115 120 125

Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys
 130 135 140

Val
 145

<210> 56
 <211> 620
 <212> DNA
 <213> Canis familiaris

<400> 56
 tatacacagt ccatatcttg aatttttagtt tcccgatttc cttgtggtga tgtccaataa 60
 gtagtttctg cccatgaact tctaacttct gatccatttg tgcattgtgc tggcagaagt 120
 gtggtttatct ttgcttcaat acctttgtta agatcaaacc catctttgta atgtagattc 180
 ttggtaatga tgggtcttcca gttttcacta tcaatgtttc ggtattttta ttcattttct 240
 attgtgcatt ccttaaaatt atccggaaat aatggagggt gccattgcaa agagagataa 300
 cctaaatata cagggtccac tatctcaaaa tcttgaggag gattaacttt tatctcagca 360
 tttgaaagca tagagccaaa tgctgtgcaa acaagcaggg tatagaggaa tccgacatcc 420
 aatgaatga aagccatttc tccaagattc aatactttga agtttccact caataatatg 480
 gtttctcaag aatgaatta tcataggcaa ttatcacagg tcctcttttt tttctcttct 540
 ccagtttgga gacattaatt agaattctta agacttcctt tcctgtctga taatcaagca 600
 cacaaactca gcctcgtgcc 620

<210> 57
 <211> 878

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(765)

<220>

<223> At location 862, n = unknown

<400> 57

caa gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac	48
Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr	
1 5 10 15	
aac tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat	96
Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His	
20 25 30	
ttt gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat	144
Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His	
35 40 45	
tca gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga	192
Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly	
50 55 60	
tgc agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc	240
Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile	
65 70 75 80	
tgt gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt	288
Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe	
85 90 95	
att ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt	336
Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu	
100 105 110	
agt ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg	384
Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met	
115 120 125	
cct aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc	432
Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe	
130 135 140	
aca gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata	480

Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly
 50 55 60

Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile
 65 70 75 80

Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe
 85 90 95

Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu
 100 105 110

Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met
 115 120 125

Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe
 130 135 140

Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile
 145 150 155 160

Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val
 165 170 175

Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu
 180 185 190

Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu
 195 200 205

Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val
 210 215 220

Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile
 225 230 235 240

Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
 245 250 255

<210> 59

<211> 878

<212> DNA

<213> Canis familiaris

<400> 59

tttttttttt tttttcnttt taaaataaga tttattcaat atttgaggaa aagcttcagt 60

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ttaataagac tcatatttaa catctggcca taagactgaa agttactgag tcaacagaat 120
gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt 180
tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaattggt 240
atcaagaaaa atactaaggt ttcccttccat atgtcacctt tccagcattg ttcactactc 300
cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360
cataattttt ggcttttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420
gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga 480
atgggtcctt taggcatggt ccatttcagg ttaatttcct ctgaattctt cacagtaaga 540
ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600
ggctctgatag gctgggattc tgatgacca ttaacacaga tgtagaaatc tttatagtct 660
gatgactcca aatagggaaa cctgcatccc atattttttc cattaacctt gatgtaatca 720
gtacactctg ctgaatggtc caagccctca taccagtaaa acaactggta attggtatca 780
aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840
cagtccatat cttgaatttt agtttcccga tttccttg 878

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<210> 60
<211> 1454
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (184)..(1341)

<220>
<223> At location 1438, n = unknown

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<400> 60
ggcacgaggc tgagtttgtg tgcttgatta tcagacagga agggaagtct tagagattct 60

aattaatgtc tccaaactgg agaagagaaa aaaaagagga cctgtgataa ttgcctatga 120

taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180

gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt 228
Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu
      1             5             10             15

gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt 276
Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val
      20             25             30

aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat 324
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
      35             40             45

ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa 372

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Leu	Ser	Leu	Gln	Trp	Gln	Pro	Pro	Leu	Phe	Pro	Asp	Asn	Phe	Lys	Glu	
		50					55					60				
tgc	aca	ata	gaa	tat	gaa	tta	aaa	tac	cga	aac	att	gat	agt	gaa	aac	420
Cys	Thr	Ile	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	
	65					70					75					
tgg	aag	acc	atc	att	acc	aag	aat	cta	cat	tac	aaa	gat	ggg	ttt	gat	468
Trp	Lys	Thr	Ile	Ile	Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	
	80				85					90					95	
ctt	aac	aaa	ggg	att	gaa	gca	aag	ata	aac	aca	ctt	ctg	cca	gca	caa	516
Leu	Asn	Lys	Gly	Ile	Glu	Ala	Lys	Ile	Asn	Thr	Leu	Leu	Pro	Ala	Gln	
				100					105					110		
tgc	aca	aat	gga	tca	gaa	gtt	aga	agt	tca	tgg	gca	gaa	act	act	tat	564
Cys	Thr	Asn	Gly	Ser	Glu	Val	Arg	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tyr	
			115					120					125			
tgg	aca	tca	cca	caa	gga	aat	cgg	gaa	act	aaa	att	caa	gat	atg	gac	612
Trp	Thr	Ser	Pro	Gln	Gly	Asn	Arg	Glu	Thr	Lys	Ile	Gln	Asp	Met	Asp	
		130					135					140				
tgt	gta	tat	tac	aac	tgg	caa	tat	tta	gtc	tgc	tct	tgg	aaa	cct	ggc	660
Cys	Val	Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	
	145					150					155					
atg	ggg	gtc	cat	ttt	gat	acc	aat	tac	cag	ttg	ttt	tac	tgg	tat	gag	708
Met	Gly	Val	His	Phe	Asp	Thr	Asn	Tyr	Gln	Leu	Phe	Tyr	Trp	Tyr	Glu	
	160				165					170					175	
ggc	ttg	gac	cat	tca	gca	gag	tgt	act	gat	tac	atc	aag	gtt	aat	gga	756
Gly	Leu	Asp	His	Ser	Ala	Glu	Cys	Thr	Asp	Tyr	Ile	Lys	Val	Asn	Gly	
				180					185					190		
aaa	aat	atg	gga	tgc	agg	ttt	ccc	tat	ttg	gag	tca	tca	gac	tat	aaa	804
Lys	Asn	Met	Gly	Cys	Arg	Phe	Pro	Tyr	Leu	Glu	Ser	Ser	Asp	Tyr	Lys	
			195					200					205			
gat	ttc	tac	atc	tgt	gtt	aat	ggg	tca	tca	gaa	tcc	cag	cct	atc	aga	852
Asp	Phe	Tyr	Ile	Cys	Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	
		210					215					220				
ccc	agc	tat	ttt	att	ttt	cag	ctt	caa	aat	ata	gtt	aaa	cct	atg	cca	900
Pro	Ser	Tyr	Phe	Ile	Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	
		225					230				235					
cca	gac	tac	ctt	agt	ctt	act	gtg	aag	aat	tca	gag	gaa	att	aac	ctg	948

[illegible]

Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu Val
1 5 10 15

Pro	Pro	Gln	Asp	Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu
		35					40					45			

Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp
65 70 75 80

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys
100 105 110

Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys
130 135 140

Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly
165 170 175

Asn	Met	Gly	Cys	Arg	Phe	Pro	Tyr	Leu	Glu	Ser	Ser	Asp	Tyr	Lys	Asp
		195					200					205			

Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro
225 230 235 240

Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys
 245 250 255

Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu
 260 265 270

Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu
 275 280 285

Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys
 290 295 300

Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile
 305 310 315 320

Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys
 325 330 335

Glu Thr Leu Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe
 340 345 350

Val Leu Val Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu
 355 360 365

Lys Thr Ile Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr
 370 375 380

Phe Cys
 385

<210> 62

<211> 1454

<212> DNA

<213> Canis familiaris

<220>

<223> At location 17, n = unknown

<400> 62

tttttttttt tttttcnttt taaaataaga tttattcaat atttgaggaa aagcttcagt 60
 ttaataagac tcatatttaa catctggcca taagactgaa agttactgag tcaacagaat 120
 gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt 180
 tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaattgt 240
 atcaagaaaa atactaaggt ttccttccat atgtcacctt tccagcattg ttcactcactc 300
 cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360
 cataattttt ggcttttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420

<210> 64
 <211> 1158
 <212> DNA
 <213> Canis familiaris

<400> 64
 acagaatgtg tcttgatgag aaaagacttc tttttttgta tgaaagatcg ttttcagtaa 60
 agccctttgc ttatacaaaa gcaggcaagt tattaccaaa acaaattattg agacaaaagc 120
 aaatggtatc aagaaaaata ctaaggtttc cttccatag tcacctttcc agcattgttc 180
 atcactccac tcaactccaga ttccatcatc tgagcaataa atattcactt tactttcttac 240
 caaaaagcat aattttttggc tttcatttga tgttcttggtg atttgtatct cattctcaac 300
 tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360
 ggctggaatg ggtccttttag gcatgttcca tttcaggtta atttcctctg aattcttcac 420
 agtaagacta aggtagtctg gtggcatagg ttttaactata ttttgaagct gaaaaataaa 480
 atagctgggt ctgataggct gggattctga tgaccatta acacagatgt agaaatcttt 540
 atagtctgat gactccaaat agggaaacct gcatcccata ttttttccat taaccttgat 600
 gtaatcagta cactctgctg aatgggtccaa gccctcatac cagtaaaaaca actggtaatt 660
 ggtatcaaaa tggacaccca tgccagggtt ccaagagcag actaaatatt gccagttgta 720
 atatacacag tccatatctt gaattttagt ttcccgattt ccttgtggtg atgtccaata 780
 agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840
 tgtgtttatc tttgcttcaa tacctttggt aagatcaaac ccatctttgt aatgtagatt 900
 cttggtaatg atggtcttcc agttttcact atcaatgttt cggatatttt attcatattc 960
 tattgtgcat tccttaaaat tatccggaaa taatggaggt tgccattgca aagagagata 1020
 acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080
 atttgaaagc atagagccaa atgctgtgca aacaagcagg gtatagagga atccgacatc 1140
 caaatgaatg aaagccat 1158

<210> 65
 <211> 1095
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(1095)

<400> 65
 tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat ttt 48
 Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
 1 5 10 15
 gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg caa 96
 Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln
 20 25 30
 cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat gaa 144
 Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu

45

act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct aaa 720
Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys

225	230	235	240	
gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca gag				768
Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu				
	245	250	255	
gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa atc				816
Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile				
	260	265	270	
aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga agt				864
Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser				
	275	280	285	
aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg agt				912
Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser				
	290	295	300	
gat gaa caa tgc tgg aaa ggt gac ata tgg aag gaa acc tta gta ttt				960
Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe				
	305	310	315	320
ttc ttg ata cca ttt gct ttt gtc tca ata ttt gtt ttg gta ata act				1008
Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr				
	325	330	335	
tgc ctg ctt ttg tat aag caa agg gct tta ctg aaa acg atc ttt cat				1056
Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His				
	340	345	350	
aca aaa aaa gaa gtc ttt tct cat caa gac aca ttc tgt				1095
Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys				
	355	360	365	

<210> 66

<211> 365

<212> PRT

<213> Canis familiaris

<400> 66

Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
1 5 10 15

Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln
20 25 30

Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu

45

Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
65 70 75 80

Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser Glu
85 90 95

Val	Arg	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Thr	Ser	Pro	Gln	Gly
			100					105					110		

Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp
115 120 125

Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe Asp
130 135 140

Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala
145 150 155 160

Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg
165 170 175

Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val
180 185 190

Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe
195 200 205

Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu
210 215 220

Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys
225 230 235 240

Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu
245 250 255

Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile
260 265 270

Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser
275 280 285

Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser

290

295

300

Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe
 305 310 315 320

Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr
 325 330 335

Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His
 340 345 350

Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
 355 360 365

<210> 67

<211> 1095

<212> DNA

<213> Canis familiaris

<400> 67

acagaatgtg tcttgatgag aaaagacttc tttttttgta tgaaagatcg ttttcagtaa 60
 agccctttgc ttatacaaaa gcaggcaagt tattaccaa acaaattattg agacaaaagc 120
 aaatggtatc aagaaaaata ctaagggtttc cttccatattg tcacctttcc agcattgttc 180
 atcactccac tcaactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 240
 caaaaagcat aattttttggc tttcatttga tgttcttggtg atttgtatct cattctcaac 300
 tgtggttagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360
 ggctggaatg ggtccttttag gcatgttcca tttcaggtta atttcctctg aattcttcac 420
 agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 480
 atagctgggt ctgataggct gggattctga tgaccatta acacagatgt agaaatcttt 540
 atagtctgat gactccaaat agggaaacct gcatcccata ttttttccat taaccttgat 600
 gtaatcagta cactctgctg aatgggtcaa gccctcatalc cagtaaaaca actggtaatt 660
 ggtatcaaaa tggacacca tgccagggtt ccaagagcag actaaatatt gccagttgta 720
 atatacacag tccatatctt gaatttttagt ttcccgattt ccttgtggtg atgtccaata 780
 agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840
 tgtgtttatc tttgcttcaa tacctttggt aagatcaaac ccatctttgt aatgtagatt 900
 cttggtaatg atggctcttc agttttcact atcaatgttt cggatattttt attcatattc 960
 tattgtgcat tccttaaaat tatccggaaa taatggaggt tgccattgca aagagagata 1020
 acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080
 atttgaaagc ataga 1095

<210> 68

<211> 954

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(954)

<400> 68

atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat 48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
1 5 10 15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg 96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
20 25 30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
35 40 45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
50 55 60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca 288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
85 90 95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa 336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac 384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
115 120 125

tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt 432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
130 135 140

gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca 480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145 150 155 160

gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc 528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
165 170 175

275

280

285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
 290 295 300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr
 305 310 315

<210> 70

<211> 954

<212> DNA

<213> Canis familiaris

<400> 70

ggtttccttc cagatatcac ctttccagca ttgttcatca ctccactcac tccagattcc 60
 atcatctgag caataaatat tcactttact tcttaccaaa aagcataatt tttggctttc 120
 atttgatgtt cttgtgattt gtatctcatt ctcaactgtg gtagtcaccc aagtagtacc 180
 atcctctgtg aattcaattt cataaatgaa acatttggct ggaatgggtc ctttaggcat 240
 gttccatttc aggttaattt cctctgaatt cttcacagta agactaaggt agtctggtgg 300
 cataggttta actatatttt gaagctgaaa aataaaatag ctgggtctga taggctggga 360
 ttctgatgac ccattaacac agatgtagaa atctttatag tctgatgact ccaaataagg 420
 aaacctgcat cccatatttt ttccattaac cttgatgtaa tcagtacact ctgctgaatg 480
 gtccaagccc tcataccagt aaaacaactg gtaattggta tcaaaatgga cacccatgcc 540
 aggtttccaa gagcagacta aatattgcc a gttgtaatat acacagtcca tatcttgaat 600
 tttagtttcc cgatttcctt gtgggtgatgt ccaataagta gtttctgccc atgaacttct 660
 aacttctgat ccatttgtgc attgtgctgg cagaagtgtg tttatctttg cttcaatacc 720
 tttgttaaga tcaaaccat ctttgtaatg tagattcttg gtaatgatgg tcttccagtt 780
 ttcactatca atgtttcggg attttaattc atattctatt gtgcattcct taaaattatc 840
 cggaaataat ggaggttgcc attgcaaaga gagataacct aaatatccag ggtccactat 900
 ctcaaaatcc tgaggaggat taacttttat ctcagcattt gaaagcatag acat 954

<210> 71

<211> 1686

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(1683)

<400> 71

atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat 48
 Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1 5 10 15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg	96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp	
20 25 30	
caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat	144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr	
35 40 45	
gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att	192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile	
50 55 60	
acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att	240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile	
65 70 75 80	
gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca	288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser	
85 90 95	
gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa	336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln	
100 105 110	
gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac	384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn	
115 120 125	
tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt	432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe	
130 135 140	
gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca	480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser	
145 150 155 160	
gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc	528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys	
165 170 175	
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt	576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys	
180 185 190	
gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att	624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile	
195 200 205	

cag tct cgt gag cag cag ttc aac ggc acc tac cgt gtg gtc agc gtc	1248
Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val	
405 410 415	
ctc ccc att gag cac cag gac tgg ctc aca ggg aag gag ttc aag tgc	1296
Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys	
420 425 430	
aga gtc aac cac ata gac ctc ccg tct ccc atc gag agg acc atc tct	1344
Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser	
435 440 445	
aag gcc aga ggg agg gcc cat aag ccc agt gtg tat gtc ctg ccg cca	1392
Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro	
450 455 460	
tcc cca aag gag ttg tca tcc agt gac aca gtc agc atc acc tgc ctg	1440
Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu	
465 470 475 480	
ata aaa gac ttc tac cca cct gac att gat gtg gag tgg cag agc aat	1488
Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn	
485 490 495	
gga cag cag gag ccc gag agg aag cac cgc atg acc ccg ccc cag ctg	1536
Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu	
500 505 510	
gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac aag	1584
Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys	
515 520 525	
agc cgc tgg cag cag gga gac ccc ttc aca tgt gcg gtg atg cat gaa	1632
Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu	
530 535 540	
act cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt	1680
Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly	
545 550 555 560	
aaa tga	1686
Lys	

<210> 72
 <211> 561
 <212> PRT
 <213> Canis familiaris

<400> 72

Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
1 5 10 15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
20 25 30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
180 185 190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
195 200 205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
210 215 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225 230 235 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr

245

250

255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
260 265 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
275 280 285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
290 295 300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305 310 315 320

Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg Cys Thr Asp
325 330 335

Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu
340 345 350

Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro
355 360 365

Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
370 375 380

Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
385 390 395 400

Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val
405 410 415

Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
420 425 430

Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
435 440 445

Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro
450 455 460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu
465 470 475 480

Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn
485 490 495

Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu

500

505

510

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
 515 520 525

Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu
 530 535 540

Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly
 545 550 555 560

Lys

<210> 73

<211> 1686

<212> DNA

<213> Canis familiaris

<400> 73

tcattttaccc ggagaatggg agaggggatag atctgtgtag tggttctgta gagtttcatg 60
 catcaccgca catgtgaagg ggtctccctg ctgccagcgg ctcttgtcca cagagagctt 120
 gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcatgc ggtgcttcct 180
 ctcgggctcc tgctgtccat tgctctgcca ctccacatca atgtcagggtg ggtagaagtc 240
 ttttatcagg caggtgatgc tgactgtgtc actggatgac aactcctttg gggatggcgg 300
 caggacatac acactgggct tatgggccct ccctctggcc ttagagatgg tcctctcgat 360
 gggagacggg aggtctatgt ggttgactct gcacttgaac tccttccctg tgagccagtc 420
 ctggtgctca atggggagga cgctgaccac acggtaggtg ccgttgaact gctgctcacg 480
 agactgggtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540
 agggtcctca cggcccagat ctaacaccac acaggtgacc tcgggtgttc gggtaatcct 600
 gaggatgtcc ttgggtttcg ggggaaagat gaggaccgaa ggccctccca gaggttcagg 660
 gactgggcat gggggtgtat cagtgcattc gcattcattg aacctgggt tgtctacttt 720
 agtgttggat ccggtttcct tccagatata acctttccag cattgttcat cactccactc 780
 actccagatt ccatcatctg agcaataaat attcacttta cttcttacca aaaagcataa 840
 tttttggctt tcatttgatg ttcttgtgat ttgtatctca ttctcaactg tggtagtcac 900
 ccaagtagta ccctcctctg tgaattcaat ttcataaatg aaacatttgg ctggaatggg 960
 tccttttaggc atgttccatt tcagggttaat ttctctgaa ttcttcacag taagactaag 1020
 gtagtctggg ggcatagggt taactatatt ttgaagctga aaaataaaaat agctgggtct 1080
 gataggctgg gattctgatg acccattaac acagatgtag aaatctttat agtctgatga 1140
 ctccaaatag ggaaacctgc atcccatatt ttttccatta accttgatgt aatcagtaca 1200
 ctctgctgaa tgggtccaagc cctcatacca gtaaaacaac tggtaattgg tatcaaaatg 1260
 gacacccatg ccagggtttcc aagagcagac taaatattgc cagttgtaat atacacagtc 1320
 catatcttga attttagttt cccgatttcc ttgtgggtgat gtccaataag tagtttctgc 1380
 ccatgaactt ctaacttctg atccatttgt gcattgtgct ggcagaagtg tgtttatctt 1440
 tgcttcaata cttttgttaa gatcaaacc atctttgtaa tgtagattct tggtaatgat 1500
 ggtcttccag ttttactat caatgtttcg gtattttaat tcatattcta ttgtgcattc 1560

cttaaaatta tccggaata atggagggtg ccattgcaaa gagagataac ctāaatatcc 1620
 aggtgccact atctcaaaat cctgaggagg attaatcttt atctcagcat ttgaaagcat 1680
 agacat 1686

<210> 74
 <211> 1698
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(1695)

<400> 74
 atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat 48
 Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1 5 10 15
 ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg 96
 Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
 20 25 30
 caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144
 Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
 35 40 45
 gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192
 Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
 50 55 60
 acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240
 Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
 65 70 75 80
 gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca 288
 Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
 85 90 95
 gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa 336
 Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
 100 105 110
 gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac 384
 Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
 115 120 125
 tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt 432

TC06040:5663360

Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Met	Gly	Val	His	Phe	
130						135					140					
gat	acc	aat	tac	cag	ttg	ttt	tac	tgg	tat	gag	ggc	ttg	gac	cat	tca	480
Asp	Thr	Asn	Tyr	Gln	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ser	
145					150					155					160	
gca	gag	tgt	act	gat	tac	atc	aag	gtt	aat	gga	aaa	aat	atg	gga	tgc	528
Ala	Glu	Cys	Thr	Asp	Tyr	Ile	Lys	Val	Asn	Gly	Lys	Asn	Met	Gly	Cys	
				165					170					175		
agg	ttt	ccc	tat	ttg	gag	tca	tca	gac	tat	aaa	gat	ttc	tac	atc	tgt	576
Arg	Phe	Pro	Tyr	Leu	Glu	Ser	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys	
			180					185					190			
gtt	aat	ggg	tca	tca	gaa	tcc	cag	cct	atc	aga	ccc	agc	tat	ttt	att	624
Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	Ile	
		195					200					205				
ttt	cag	ctt	caa	aat	ata	gtt	aaa	cct	atg	cca	cca	gac	tac	ctt	agt	672
Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	Pro	Asp	Tyr	Leu	Ser	
	210					215						220				
ctt	act	gtg	aag	aat	tca	gag	gaa	att	aac	ctg	aaa	tgg	aac	atg	cct	720
Leu	Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	Lys	Trp	Asn	Met	Pro	
225					230					235				240		
aaa	gga	ccc	att	cca	gcc	aaa	tgt	ttc	att	tat	gaa	att	gaa	ttc	aca	768
Lys	Gly	Pro	Ile	Pro	Ala	Lys	Cys	Phe	Ile	Tyr	Glu	Ile	Glu	Phe	Thr	
				245					250					255		
gag	gat	ggt	act	act	tgg	gtg	act	acc	aca	gtt	gag	aat	gag	ata	caa	816
Glu	Asp	Gly	Thr	Thr	Trp	Val	Thr	Thr	Thr	Val	Glu	Asn	Glu	Ile	Gln	
			260					265					270			
atc	aca	aga	aca	tca	aat	gaa	agc	caa	aaa	tta	tgc	ttt	ttg	gta	aga	864
Ile	Thr	Arg	Thr	Ser	Asn	Glu	Ser	Gln	Lys	Leu	Cys	Phe	Leu	Val	Arg	
		275						280				285				
agt	aaa	gtg	aat	att	tat	tgc	tca	gat	gat	gga	atc	tgg	agt	gag	tgg	912
Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp	
	290					295				300						
agt	gat	gaa	caa	tgc	tgg	aaa	ggt	gat	atc	tgg	aag	gaa	acc	gga	tcc	960
Ser	Asp	Glu	Gln	Cys	Trp	Lys	Gly	Asp	Ile	Trp	Lys	Glu	Thr	Gly	Ser	
305					310					315				320		
aac	act	aaa	gta	gac	aag	cca	gtg	ccc	aaa	aga	gaa	aat	gga	aga	gtt	1008

Asn Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val	
325 330 335	
cct cgc cca cct gat tgt ccc aaa tgc cca gcc cct gaa atg ctg gga	1056
Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly	
340 345 350	
ggg cct tgc gtc ttc atc ttt ccc ccg aaa ccc aag gac acc ctg ttg	1104
Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu	
355 360 365	
att gcc cga aca cct gag gtc aca tgt gtg gtg gtg gat ctg gac cca	1152
Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro	
370 375 380	
gaa gac cct gag gtg cag atc agc tgg ttc gtg gac ggt aag cag atg	1200
Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met	
385 390 395 400	
caa aca gcc aag act cag cct cgt gag gag cag ttc aat ggc acc tac	1248
Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr	
405 410 415	
cgt gtg gtc agt gtc ctg ccc att ggg cac cag gac tgg ctg aag ggg	1296
Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly	
420 425 430	
aag cag ttc acg tgc aaa gtc aac aac aaa gcc ctg cca tcc ccg atc	1344
Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile	
435 440 445	
gag agg acc atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg	1392
Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val	
450 455 460	
tat gtc ctg ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc	1440
Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser	
465 470 475 480	
ttg aca tgc ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag	1488
Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu	
485 490 495	
tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc acg acc	1536
Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr	
500 505 510	
ccg ccc cag ctg gac gag gag ggg tcc tac ttc ctg tac agc aag ctg	1584

Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu
 515 520 525

tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg 1632
 Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala
 530 535 540

gtg atg cat gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc 1680
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser
 545 550 555 560

cat tct ccg ggt aaa tga 1698
 His Ser Pro Gly Lys
 565

<210> 75
 <211> 565
 <212> PRT
 <213> Canis familiaris

<400> 75
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Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
 20 25 30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
 35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
 50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
 65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
 85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
 100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
 115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
 130 135 140

Time	Lat	Long	Alt	Temp	Hum	Wind	Dir	Speed	Pressure	Clouds	Visibility	Remarks
0000	10° 00' N	100° 00' W	1000	25.0	80	10	090	10	1013.2	0	10	Clear
0100	10° 05' N	100° 05' W	1000	25.5	80	10	090	10	1013.2	0	10	Clear
0200	10° 10' N	100° 10' W	1000	26.0	80	10	090	10	1013.2	0	10	Clear
0300	10° 15' N	100° 15' W	1000	26.5	80	10	090	10	1013.2	0	10	Clear
0400	10° 20' N	100° 20' W	1000	27.0	80	10	090	10	1013.2	0	10	Clear
0500	10° 25' N	100° 25' W	1000	27.5	80	10	090	10	1013.2	0	10	Clear
0600	10° 30' N	100° 30' W	1000	28.0	80	10	090	10	1013.2	0	10	Clear
0700	10° 35' N	100° 35' W	1000	28.5	80	10	090	10	1013.2	0	10	Clear
0800	10° 40' N	100° 40' W	1000	29.0	80	10	090	10	1013.2	0	10	Clear
0900	10° 45' N	100° 45' W	1000	29.5	80	10	090	10	1013.2	0	10	Clear
1000	10° 50' N	100° 50' W	1000	30.0	80	10	090	10	1013.2	0	10	Clear
1100	10° 55' N	100° 55' W	1000	30.5	80	10	090	10	1013.2	0	10	Clear
1200	11° 00' N	101° 00' W	1000	31.0	80	10	090	10	1013.2	0	10	Clear
1300	11° 05' N	101° 05' W	1000	31.5	80	10	090	10	1013.2	0	10	Clear
1400	11° 10' N	101° 10' W	1000	32.0	80	10	090	10	1013.2	0	10	Clear
1500	11° 15' N	101° 15' W	1000	32.5	80	10	090	10	1013.2	0	10	Clear
1600	11° 20' N	101° 20' W	1000	33.0	80	10	090	10	1013.2	0	10	Clear
1700	11° 25' N	101° 25' W	1000	33.5	80	10	090	10	1013.2	0	10	Clear
1800	11° 30' N	101° 30' W	1000	34.0	80	10	090	10	1013.2	0	10	Clear
1900	11° 35' N	101° 35' W	1000	34.5	80	10	090	10	1013.2	0	10	Clear
2000	11° 40' N	101° 40' W	1000	35.0	80	10	090	10	1013.2	0	10	Clear
2100	11° 45' N	101° 45' W	1000	35.5	80	10	090	10	1013.2	0	10	Clear
2200	11° 50' N	101° 50' W	1000	36.0	80	10	090	10	1013.2	0	10	Clear
2300	11° 55' N	101° 55' W	1000	36.5	80	10	090	10	1013.2	0	10	Clear

Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr
405 410 415

Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly
420 425 430

Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile
435 440 445

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
450 455 460

Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser
465 470 475 480

Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu
485 490 495

Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr
500 505 510

Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu
515 520 525

Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala
530 535 540

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser
545 550 555 560

His Ser Pro Gly Lys
565

<210> 76

<211> 1698

<212> DNA

<213> Canis familiaris

<400> 76

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gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcgtgc ggtacttgct 180
ctcaggctcc tgctgtccat tgctctgccca ctccacatca atgtcagggtg ggaagaagtc 240
tttgatcagg catgtcaagc tgactgtgtt cttgctcaac tcctccccggg atggcggcag 300
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<222> (1) .. (1689)
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88

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Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr
465 470 475 480

tgt ctg gtc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag 1488
Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln
485 490 495

agc aat gga cag cag gag cct gag agc aag tac cgc atg acc ccg ccc 1536
Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro
500 505 510

cag ctg gat gaa gat ggg tcc tac ttc cta tac agc aag ctc tcc gtg 1584
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
515 520 525

gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg 1632
Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met
530 535 540

cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct 1680
His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser
545 550 555 560

ccg ggt aaa tga	1692
Pro Gly Lys	

<211> 563

<212> PRT

<213> Canis familiaris

<400> 78

Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
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Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp

20 25 30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr

35

40

45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
180 185 190

Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	Ile
		195					200					205			

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
210 215 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225 230 235 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
245 250 255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
260 265 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
275 280 285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp

290		295		300															
Ser	Asp	Glu	Gln	Cys	Trp	Lys	Gly	Asp	Ile	Trp	Lys	Glu	Thr	Gly	Ser				
305					310					315					320				
Asn	Thr	Lys	Val	Asp	Lys	Pro	Val	Ala	Lys	Glu	Cys	Glu	Cys	Lys	Cys				
				325					330					335					
Asn	Cys	Asn	Asn	Cys	Pro	Cys	Pro	Gly	Cys	Gly	Leu	Leu	Gly	Gly	Pro				
				340				345					350						
Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Ile	Leu	Val	Thr	Ala				
		355					360					365							
Arg	Thr	Pro	Thr	Val	Thr	Cys	Val	Val	Val	Asp	Leu	Asp	Pro	Glu	Asn				
370						375					380								
Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Ser	Lys	Gln	Val	Gln	Thr				
385					390					395					400				
Ala	Asn	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Ser	Asn	Gly	Thr	Tyr	Arg	Val				
				405					410					415					
Val	Ser	Val	Leu	Pro	Ile	Gly	His	Gln	Asp	Trp	Leu	Ser	Gly	Lys	Gln				
			420					425					430						
Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ser	Pro	Ile	Glu	Glu				
		435					440					445							
Ile	Ile	Ser	Lys	Thr	Pro	Gly	Gln	Ala	His	Gln	Pro	Asn	Val	Tyr	Val				
450						455					460								
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Met	Ser	Lys	Asn	Thr	Val	Thr	Leu	Thr				
465					470					475					480				
Cys	Leu	Val	Lys	Asp	Phe	Phe	Pro	Pro	Glu	Ile	Asp	Val	Glu	Trp	Gln				
				485					490					495					
Ser	Asn	Gly	Gln	Gln	Glu	Pro	Glu	Ser	Lys	Tyr	Arg	Met	Thr	Pro	Pro				
		500						505					510						
Gln	Leu	Asp	Glu	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Ser	Val				
		515						520				525							
Asp	Lys	Ser	Arg	Trp	Gln	Arg	Gly	Asp	Thr	Phe	Ile	Cys	Ala	Val	Met				
530						535					540								
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Ile	Ser	Leu	Ser	His	Ser				

545

550

555

560

Pro Gly Lys

<210> 79

<211> 1692

<212> DNA

<213> Canis familiaris

<400> 79

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gctgtatagg aagtaggacc catcttcate cagctggggc ggggtcatgc ggtacttgct 180
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gttttctggg tccagatcca ccaccacaca agtgactgtg ggtgtccggg cagtcacgag 600
gatgtccttg ggttttgggg gaaagatgaa gaccgaaggc cctcccagca ggccacaacc 660
tgggcatggg cagttgttac agttacactt gcactcgcat tctttggcca ctggcttgct 720
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<210> 80

<211> 1686

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(1683)

<400> 80

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ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg	96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp	
20 25 30	
caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat	144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr	
35 40 45	
gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att	192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile	
50 55 60	
acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att	240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile	
65 70 75 80	
gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca	288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser	
85 90 95	
gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa	336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln	
100 105 110	
gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac	384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn	
115 120 125	
tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt	432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe	
130 135 140	
gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca	480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser	
145 150 155 160	
gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc	528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys	

	165	170	175	
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt				576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys				
	180	185	190	
gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att				624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile				
	195	200	205	
ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt				672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser				
	210	215	220	
ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct				720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro				
	225	230	235	240
aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca				768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr				
	245	250	255	
gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa				816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln				
	260	265	270	
atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga				864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg				
	275	280	285	
agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg				912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp				
	290	295	300	
agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc				960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser				
	305	310	315	320
aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc aag tgt				1008
Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys				
	325	330	335	
ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg gtc ttc				1056
Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe				
	340	345	350	
atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc				1104
Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro				

545

550

555

560

aaa tga

1686

Lys

<210> 81

<211> 561

<212> PRT

<213> Canis familiaris

<400> 81

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Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
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Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
 35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
 50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
 65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
 85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
 100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
 115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
 130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
 145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
 165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
 180 185 190

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 ctctgctgaa tgggtccaagc cctcatacca gtaaaacaac tggtaattgg tatcaaaatg 1260
 gacacccatg ccagggtttcc aagagcagac taaatattgc cagttgtaat atacacagtc 1320
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 ggtcttccag ttttcaactat caatgtttcg gtattttaat tcatattcta ttgtgcattc 1560
 cttaaaatta tccggaaata atggagggtt ccattgcaaa gagagataac ctaaatatcc 1620
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<210> 83

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<220>

<223> At locations 9, 18, 21 and 27, n = unknown

<400> 83

athtggacnt ggaayccncc ngarggngc 29

<210> 84

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<220>

<223> At locations 6, 9, 21 and 33, n = unknown

<400> 84

atyttncng crttrtctyt naccatdaty tgnac 35

<210> 85

<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<220>
<223> At locations 12, 18 and 21, n = unknown

<400> 85
garathaarg tnaayccncc ncargaytty garat

35

<210> 86
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<220>
<223> At locations 12, 22 and 31, n = unknown

<400> 86
tayaargayg gnttctgayy tnaayaargg nathga

36

<210> 87
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<220>
<223> At locations 7, 16, 25 and 40, n = unknown

<400> 87
ccaytcnswc cadatncert crtngcrca rtadatrttn acytt

45

<210> 88

<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<220>

<223> At locations 9 and 12, n = unknown

<400> 88

gertgrtcna rnccytcrta cca

23

<210> 89

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 89

agcggatccc tctatgcttt caaatgctga gataaaagtt aatcctcctc agg

53

<210> 90

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 90

tggacatcac cacaaggaaa tcggg

25

<210> 91

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer

<400> 91
gcacatatgt ctatgctttc aaatgctgaa taaaagttaa tcctcctcag g 51

<210> 92
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 92
aaaggatccg gtttccttcc agatatcatt tccagc 36

<210> 93
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 93
ccgggatcca acactaaagt agacaagcgt g 31

<210> 94
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 94
gcgctcgagt catttaccg gagaatggga ggg 33

<210> 95
<211> 1525
<212> DNA

<213> Canis familiaris

<400> 95

gaattcggca cgaggggagag gaggagggaa agatagaaag agagagagaa agattgcttg 60
ctaccctga acagtacct ctctcaagac agtgctttgc tcttcacgta taaggaagga 120
aaacagtaga gattcaattt agtgtctaag gtggaaagga ggacaaagag gtcttgtgat 180
aactgcctgt gataatacat ttcttgagaa accatattat tgagtagagc ttccagcaca 240
ctaaatcctg gagaaatggc ttttgtgcat atcagatgct tgtgtttcat tcttctttgt 300
acaataactg gctattcttt ggagataaaa gttaatcctc ctcaggattt tgaaatattg 360
gacctcggat tacttggtta tctctatttg caatggaaac ctccctgtggg tatagaaaaa 420
tttaagggct gtacactaga atatgagtta aaataccgaa atgttgatag cgacagctgg 480
aagactataa ttactaggaa tctaatttac aaggatgggt ttgatcttaa taaaggcatt 540
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ccatggatag aagcttctta tgggatatca gatgaaggaa gtttggaac taaaattcag 660
gacatgaagt gtatatatta taactggcag tatttgggtc gctcttgga acctggcaag 720
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gtggagaagg aagaacctga acccacattg agcctccatg tggatctgaa caaagaagtg 1380
tgtgcttatg aagataccct ctgttaaacc accaatttct tgacatagag ccagccagca 1440
ggagtcatat taaactcaat ttctcttaaa atttcgaata catcttcttg aaaatccaaa 1500
aaaaaaaaa aaaaaaaaaa tcgag 1525

<210> 96

<211> 1369

<212> DNA

<213> Canis familiaris

<400> 96

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gctatcggat gcttatatac ctttctgata agcacaacat ttggctgtac ttcatcttca 180
gacaccgaga taaaagttaa cctcctcag gattttgaga tagtggatcc cggatactta 240
ggttatctct atttgcaatg gcaaccccca ctgtctctgg atcattttta ggaatgcaca 300
gtggaatatg aactaaaata ccgaaacatt ggtagtgaag catggaagac catcattact 360
aagaatctac attacaaaga tgggtttgat cttaacaagg gcattgaagc gaagatacac 420
acgcttttac catggcaatg cacaatgga tcagaagttc aaagttcctg ggcagaaact 480
acttattgga tatcaccaca aggaattcca gaaactaaag ttcaggatat ggattgcgta 540
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accaattaca acttggtttta ctggtatgag ggcttggatc atgcattaca gtgtgttgat 660

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tatttcactt ttcagcttca aaatatagtt aaacctttgc cgccagtcta tcttactttt 840
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agagacatgg tattgactca acagtttcca gtcattggca aatgttcaat atgagtctca 1320
ataaactgaa tttttcttgc gaaaaaaaaa aaaaaaatc cgcggatcc 1369
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<210> 97

<211> 1525

<212> DNA

<213> Canis familiaris

<400> 97

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aacagagggg atcttcataa gcacacactt ctttgctcag atccacatgg aggtcattat 180
tggtgtcagg ttcttccttc tccacaataa ggcaaagaag taacaaaagg aatataaaga 240
aaagacaaac tggactatg aaaataatct ttgagtctgg ccctgtgtaa ctttcccaac 300
attcctcttc actccattcg ctccaaatc catcatctgc acaatatata ttgaccttac 360
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ttttgtctgt ggcagactcc caggaaatat cgtcttctcg gatcacaatt tcataagtgt 480
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tatagttggg atcagaatat actgtcttgc cagggttcca agagcagacc aaatactgcc 840
agttataata tatacacttc atgtcctgaa ttttagtttc caaacttcct tcatctgata 900
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acactaaatt gaatctctac tgttttctct ccttatacgt gaagagcaaa gcaactgtct 1440
gagagaggtc actgttcagg ggtagcaagc aatctttctc tctctcttct tatctttccc 1500
tctcctctc cctcgtgccg aattc 1525
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<210> 98
 <211> 1369
 <212> DNA
 <213> Canis familiaris

<400> 98
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 gtcttcatgt atcacagaaa aattctggaa tcatttttgg gtaggtgttt ggcttacgca 180
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 tccaaattcc gtcacttgag caataaatat tcactttgct tcttactaca aagcataatt 360
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 aagccatttc tccgagattt aaaaccttga tattgcctct ctccccgccg acaggcacac 1320
 ttctgaccag gttatggcga cttcaaatag cttcatccg cgcggatcc 1369

<210> 99
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<400> 99
 ctctactatt ggcacagcag cctggga

27

<210> 100
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 100

agtcagagca aaggaacaac caatgtg

27

<210> 101

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 101

cctcccgagg gagccagccc g

21

<210> 102

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 102

cgggctggct ccctcgggag g

21

<210> 103

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 103

catggtcccc ggcgttcttc c

21

<210> 104

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 104

ggtgagaata ccgacccac g

21

109